



IFWO

## RAW SEQUENCE LISTING

DATE: 02/20/2004

PATENT APPLICATION: US/10/632,150

TIME: 12:37:32

Input Set : N:\Crf3\RULE60\10632150.RAW.txt

Output Set: N:\CRF4\02202004\J632150.raw

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1 <110> APPLICANT: Chiaur, D.
2     Pagano, M.
3     Latres, E.
4 <120> TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
5 <130> FILE REFERENCE: 5914-081
6 <140> CURRENT APPLICATION NUMBER: 10/632,150
7 <141> CURRENT FILING DATE: 2003-07-30
8 <150> PRIOR APPLICATION NUMBER: US/09/385,219
9 <151> PRIOR FILING DATE: 1999-08-27
10 <150> PRIOR APPLICATION NUMBER: 60/098,355
11 <151> PRIOR FILING DATE: 1998-08-28
12 <150> PRIOR APPLICATION NUMBER: 60/118,568
13 <151> PRIOR FILING DATE: 1999-02-03
14 <150> PRIOR APPLICATION NUMBER: 60/124,449
15 <151> PRIOR FILING DATE: 1999-03-15
16 <160> NUMBER OF SEQ ID NOS: 90
17 <170> SOFTWARE: PatentIn Ver. 2.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 2151
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
23 <400> SEQUENCE: 1
24     tgcgttggtc gcggcctggc accaaagggg cggccccggc ggagagcgga cccagtggcc 60
25     tcggcgatta tggaccggc cgaggcgggt ctgcaagaga aggcactcaa gtttatgaat 120
26     tcctcagaga gagaagactg taataatggc gaaccccccta ggaagataat accagagaag 180
27     aattcacitg gacagacata caacagctgt gccagactct gcttaaacca agaaacagta 240
28     tgtttagcaa gcactgctat gaagactgag aattgtgtgg ccaaaacaaa acttgccaat 300
29     ggcaattcca gtatgattgt gcccaagcaa cggaaactct cagcaagcta tgaaaaggaa 360
30     aaggaactgt gtgtcaaata ctttgagcag tggtcagagt cagatcaagt ggaatttgtg 420
31     gaacatctta tatcccaaat gtgtcattac caacatgggc acataaactc gtatcttaaa 480
32     cctatgttgc agagagattt cataactgct ctgccagctc ggggattgga tcatatcgct 540
33     gagaacattc tgtcatacct ggatgccaaa tcaactatgt ctgctgaact tgtgtgcaag 600
34     gaatggtacc gagtgacctc tgatggcatg ctgtggaaga agcttatcga gagaatggtc 660
35     aggacagatt ctctgtggag aggcctggca gaacgaagag gatggggaca gtatttattc 720
36     aaaaacaaac ctctgacgg gaatgctcct cccaactctt tttatagagc actttatcct 780
37     aaaattatac aagacattga gacaatagaa tctaattgga gatgtggaag acatagttta 840
38     cagagaattc actgccgaag tgaaacaagc aaaggagttt actgtttaca gtatgatgat 900
39     cagaaaatag taagcggcct tcgagacaac acaatcaaga tctgggataa aaacacattg 960
40     gaatgcaagc gaattctcac aggccataca ggttcagtc tctgtctcca gtatgatgat 1020
41     agagtgatca taacaggatc atcggattcc acggtcagag tgtgggatgt aaatacaggt 1080
42     gaaatgctaa acacgttgat tcaccattgt gaagcagttc tgcacttgcg tttcaataat 1140
43     ggcatgatgg tgacctgctc caaagatcgt tcattgctg tatgggatat ggcctcccca 1200
44     actgacatta ccctccggag ggtgctggtc ggacaccgag ctgctgtcaa tgtttagtag 1260

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45      tttgatgaca agtacattgt ttctgcatct ggggatagaa ctataaaggt atggaacaca 1320
46      agtacttggtg aatttgtaag gaccttaaat ggacacaaac gaggcattgc ctgtttgcag 1380
47      tacagggaca ggctggtagt gaggggctca tctgacaaca ctatcagatt atgggacata 1440
48      gaatgtggtg catgttttacg agtggttagaa ggccatgagg aattggtgcg ttgtattcga 1500
49      tttgataaca agaggatagt cagtggggcc tatgatggaa aaattaaagt gtgggatctt 1560
50      gtggctgctt tggacccccg tgctcctgca gggacactct gtctacggac ccttgtggag 1620
51      cattccggaa gagtttttcg actacagttt gatgaattcc agattgtcag tagttcacat 1680
52      gatgacacaa tcctcatctg ggacttccta aatgatccag ctgcccagc tgaaccccc 1740
53      cgttccccctt ctcgaacata cacctacatc tccagataaa taaccataca ctgacctcat 1800
54      acttgcccag gaccatttaa agttgcggta tttaacgtat ctgccaatac caggatgagc 1860
55      aacaacagta acaatcaaac tactgcccag tttccctgga ctagccgagg agcagggctt 1920
56      tgagactcct gttgggacac agttggtctg cagtcggccc aggacggtct actcagcaca 1980
57      actgactgct tcagtgtctg tatcagaaga tgtcttctat caattgtgaa tgattggaac 2040
58      ttttaaacct cccctcctct cctcctttca cctctgcacc tagtttttcc ccattgggtc 2100
59      cagacaaagg tgacttataa atatatttag tgttttgcca gaaaaaaaa a 2151

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61 &lt;210&gt; SEQ ID NO: 2

62 &lt;211&gt; LENGTH: 569

63 &lt;212&gt; TYPE: PRT

64 &lt;213&gt; ORGANISM: Homo sapiens

65 &lt;400&gt; SEQUENCE: 2

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66      Met Asp Pro Ala Glu Ala Val Leu Gln Glu Lys Ala Leu Lys Phe Met
67      1          5          10          15
68      Asn Ser Ser Glu Arg Glu Asp Cys Asn Asn Gly Glu Pro Pro Arg Lys
69      20          25          30
70      Ile Ile Pro Glu Lys Asn Ser Leu Arg Gln Thr Tyr Asn Ser Cys Ala
71      35          40          45
72      Arg Leu Cys Leu Asn Gln Glu Thr Val Cys Leu Ala Ser Thr Ala Met
73      50          55          60
74      Lys Thr Glu Asn Cys Val Ala Lys Thr Lys Leu Ala Asn Gly Thr Ser
75      65          70          75          80
76      Ser Met Ile Val Pro Lys Gln Arg Lys Leu Ser Ala Ser Tyr Glu Lys
77      85          90          95
78      Glu Lys Glu Leu Cys Val Lys Tyr Phe Glu Gln Trp Ser Glu Ser Asp
79      100          105          110
80      Gln Val Glu Phe Val Glu His Leu Ile Ser Gln Met Cys His Tyr Gln
81      115          120          125
82      His Gly His Ile Asn Ser Tyr Leu Lys Pro Met Leu Gln Arg Asp Phe
83      130          135          140
84      Ile Thr Ala Leu Pro Ala Arg Gly Leu Asp His Ile Ala Glu Asn Ile
85      145          150          155          160
86      Leu Ser Tyr Leu Asp Ala Lys Ser Leu Cys Ala Ala Glu Leu Val Cys
87      165          170          175
88      Lys Glu Trp Tyr Arg Val Thr Ser Asp Gly Met Leu Trp Lys Lys Leu
89      180          185          190
90      Ile Glu Arg Met Val Arg Thr Asp Ser Leu Trp Arg Gly Leu Ala Glu
91      195          200          205
92      Arg Arg Gly Trp Gly Gln Tyr Leu Phe Lys Asn Lys Pro Pro Asp Gly
93      210          215          220
94      Asn Ala Pro Pro Asn Ser Phe Tyr Arg Ala Leu Tyr Pro Lys Ile Ile

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95      225      230      235      240
96  Gln Asp Ile Glu Thr Ile Glu Ser Asn Trp Arg Cys Gly Arg His Ser
97      245      250      255
98  Leu Gln Arg Ile His Cys Arg Ser Glu Thr Ser Lys Gly Val Tyr Cys
99      260      265      270
100  Leu Gln Tyr Asp Asp Gln Lys Ile Val Ser Gly Leu Arg Asp Asn Thr
101      275      280      285
102  Ile Lys Ile Trp Asp Lys Asn Thr Leu Glu Cys Lys Arg Ile Leu Thr
103      290      295      300
104  Gly His Thr Gly Ser Val Leu Cys Leu Gln Tyr Asp Glu Arg Val Ile
105      305      310      315      320
106  Ile Thr Gly Ser Ser Asp Ser Thr Val Arg Val Trp Asp Val Asn Thr
107      325      330      335
108  Gly Glu Met Leu Asn Thr Leu Ile His His Cys Glu Ala Val Leu His
109      340      345      350
110  Leu Arg Phe Asn Asn Gly Met Met Val Thr Cys Ser Lys Asp Arg Ser
111      355      360      365
112  Ile Ala Val Trp Asp Met Ala Ser Pro Thr Asp Ile Thr Leu Arg Arg
113      370      375      380
114  Val Leu Val Gly His Arg Ala Ala Val Asn Val Val Asp Phe Asp Asp
115      385      390      395      400
116  Lys Tyr Ile Val Ser Ala Ser Gly Asp Arg Thr Ile Lys Val Trp Asn
117      405      410      415
118  Thr Ser Thr Cys Glu Phe Val Arg Thr Leu Asn Gly His Lys Arg Gly
119      420      425      430
120  Ile Ala Cys Leu Gln Tyr Arg Asp Arg Leu Val Val Ser Gly Ser Ser
121      435      440      445
122  Asp Asn Thr Ile Arg Leu Trp Asp Ile Glu Cys Gly Ala Cys Leu Arg
123      450      455      460
124  Val Leu Glu Gly His Glu Glu Leu Val Arg Cys Ile Arg Phe Asp Asn
125      465      470      475      480
126  Lys Arg Ile Val Ser Gly Ala Tyr Asp Gly Lys Ile Lys Val Trp Asp
127      485      490      495
128  Leu Val Ala Ala Leu Asp Pro Arg Ala Pro Ala Gly Thr Leu Cys Leu
129      500      505      510
130  Arg Thr Leu Val Glu His Ser Gly Arg Val Phe Arg Leu Gln Phe Asp
131      515      520      525
132  Glu Phe Gln Ile Val Ser Ser Ser His Asp Asp Thr Ile Leu Ile Trp
133      530      535      540
134  Asp Phe Leu Asn Asp Pro Ala Ala Gln Ala Glu Pro Pro Arg Ser Pro
135      545      550      555      560
136  Ser Arg Thr Tyr Thr Tyr Ile Ser Arg
137      565
139 <210> SEQ ID NO: 3
140 <211> LENGTH: 1476
141 <212> TYPE: DNA
142 <213> ORGANISM: Homo sapiens
143 <400> SEQUENCE: 3
144  atggagagaa aggactttga gacatggctt gataacattt ctgttacatt tcttttctctg 60

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## RAW SEQUENCE LISTING

DATE: 02/20/2004

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TIME: 12:37:32

Input Set : N:\Crif3\RULE60\10632150.RAW.txt

Output Set: N:\CRF4\02202004\J632150.raw

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145 acggacttgc agaaaaaatga aactctggat cacctgatta gtctgagtgg ggcagtccag 120
146 ctccaggcatc tctccaataa cctagagact ctctcaagc gggacttcct caaactcctt 180
147 cccctggagc tcagttttta tttgttaaaa tggctcgatc ctccagacttt actcacatgc 240
148 tgccctcgtct ctaaacagtg gaataagggtg ataagtgcct gtacagaggt gtggcagact 300
149 gcatgtaaaaa atttgggctg gcagatagat gattctgttc aggacgcttt gcactggaag 360
150 aaggtttatt tgaaggctat tttgagaatg aagcaactgg aggaccatga agcctttgaa 420
151 acctcgtcat taattggaca cagtgccaga gtgtatgcac tttactacaa agatggactt 480
152 ctctgtacag ggtcagatga ctgtctgca aagctgtggg atgtgagcac agggcagtgc 540
153 gtttatggca tccagaccca cacttgtagc gcggtgaagt ttgatgaaca gaagcttgtg 600
154 acaggctcct ttgacaacac tgtggcttgc tgggaatgga gttccggagc caggaccag 660
155 cactttcggg ggcacacggg ggcggtatct agcgtggact acaatgatga actggatgc 720
156 ttggtgagcg gctctgcaga ctctactgtg aaagtatggg ctttatctgc tgggacatgc 780
157 ctgaacacac tcaccgggca caccgaatgg gtcaccaagg tagttttgca gaagtgcaa 840
158 gtcaagtctc tcttgacag tcttgagagac tacatcctct taagtgcaga caaatatgag 900
159 attaagattt ggccaattgg gagagaaatc aactgtaagt gcttaaagac attgtctgtc 960
160 tctgaggata gaagtatctg cctgcagcca agacttcatt ttgatggcaa atacattgtc 1020
161 ttagttcag cacttggctc ctaccagtgg gactttgcca gttatgatat tctcagggtc 1080
162 atcaagactc ctgagatagc aaacttggcc ttgcttggct ttggagatat ctttgcctg 1140
163 ctgtttgaca accgctacct gtacatcatg gacttgcgga cagagagcct gattagtcgc 1200
164 tggcctctgc cagagtacag ggaatcaaag agaggctcaa gcttcttggc aggcgaacat 1260
165 cctggctgaa tggactggat gggcacaatg acacgggctt ggtctttgcc accagcatgc 1320
166 ctgaccacag tattcacctg gtgttgtgga aggagcacgg ctgacaccat gagccaccac 1380
167 cgctgactga ctttgggtgc cggggctgcg ggttttgggt gcacctctgc ggcacgcgac 1440
168 tgcatgaacc aaagtctca cctaattgta tcatca 1476

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170 &lt;210&gt; SEQ ID NO: 4

171 &lt;211&gt; LENGTH: 422

172 &lt;212&gt; TYPE: PRT

173 &lt;213&gt; ORGANISM: Homo sapiens

174 &lt;400&gt; SEQUENCE: 4

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175 Met Glu Arg Lys Asp Phe Glu Thr Trp Leu Asp Asn Ile Ser Val Thr
176 1 5 10 15
177 Phe Leu Ser Leu Thr Asp Leu Gln Lys Asn Glu Thr Leu Asp His Leu
178 20 25 30
179 Ile Ser Leu Ser Gly Ala Val Gln Leu Arg His Leu Ser Asn Asn Leu
180 35 40 45
181 Glu Thr Leu Leu Lys Arg Asp Phe Leu Lys Leu Leu Pro Leu Glu Leu
182 50 55 60
183 Ser Phe Tyr Leu Leu Lys Trp Leu Asp Pro Gln Thr Leu Leu Thr Cys
184 65 70 75 80
185 Cys Leu Val Ser Lys Gln Trp Asn Lys Val Ile Ser Ala Cys Thr Glu
186 85 90 95
187 Val Trp Gln Thr Ala Cys Lys Asn Leu Gly Trp Gln Ile Asp Asp Ser
188 100 105 110
189 Val Gln Asp Ala Leu His Trp Lys Lys Val Tyr Leu Lys Ala Ile Leu
190 115 120 125
191 Arg Met Lys Gln Leu Glu Asp His Glu Ala Phe Glu Thr Ser Ser Leu
192 130 135 140
193 Ile Gly His Ser Ala Arg Val Tyr Ala Leu Tyr Tyr Lys Asp Gly Leu
194 145 150 155 160

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195   Leu Cys Thr Gly Ser Asp Asp Leu Ser Ala Lys Leu Trp Asp Val Ser
196               165                      170                      175
197   Thr Gly Gln Cys Val Tyr Gly Ile Gln Thr His Thr Cys Ala Ala Val
198               180                      185                      190
199   Lys Phe Asp Glu Gln Lys Leu Val Thr Gly Ser Phe Asp Asn Thr Val
200               195                      200                      205
201   Ala Cys Trp Glu Trp Ser Ser Gly Ala Arg Thr Gln His Phe Arg Gly
202               210                      215                      220
203   His Thr Gly Ala Val Phe Ser Val Asp Tyr Asn Asp Glu Leu Asp Ile
204               225                      230                      235                      240
205   Leu Val Ser Gly Ser Ala Asp Phe Thr Val Lys Val Trp Ala Leu Ser
206               245                      250                      255
207   Ala Gly Thr Cys Leu Asn Thr Leu Thr Gly His Thr Glu Trp Val Thr
208               260                      265                      270
209   Lys Val Val Leu Gln Lys Cys Lys Val Lys Ser Leu Leu His Ser Pro
210               275                      280                      285
211   Gly Asp Tyr Ile Leu Leu Ser Ala Asp Lys Tyr Glu Ile Lys Ile Trp
212               290                      295                      300
213   Pro Ile Gly Arg Glu Ile Asn Cys Lys Cys Leu Lys Thr Leu Ser Val
214               305                      310                      315                      320
215   Ser Glu Asp Arg Ser Ile Cys Leu Gln Pro Arg Leu His Phe Asp Gly
216               325                      330                      335
217   Lys Tyr Ile Val Cys Ser Ser Ala Leu Gly Leu Tyr Gln Trp Asp Phe
218               340                      345                      350
219   Ala Ser Tyr Asp Ile Leu Arg Val Ile Lys Thr Pro Glu Ile Ala Asn
220               355                      360                      365
221   Leu Ala Leu Leu Gly Phe Gly Asp Ile Phe Ala Leu Leu Phe Asp Asn
222               370                      375                      380
223   Arg Tyr Leu Tyr Ile Met Asp Leu Arg Thr Glu Ser Leu Ile Ser Arg
224               385                      390                      395                      400
225   Trp Pro Leu Pro Glu Tyr Arg Glu Ser Lys Arg Gly Ser Ser Phe Leu
226               405                      410                      415
227   Ala Gly Glu His Pro Gly
228               420
230 <210> SEQ ID NO: 5
231 <211> LENGTH: 1407
232 <212> TYPE: DNA
233 <213> ORGANISM: Homo sapiens
234 <400> SEQUENCE: 5
235   cggggtggtg tgtgggggaa gccgcccccg gcagcaggat gaaacgagga ggaagagata 60
236   gtgaccgtaa ttcacagaa gaaggaactg cagagaaatc caagaaactg aggactacaa 120
237   atgagcattc tcagacttgt gattggggta atctccttca ggacattatt ctccaagtat 180
238   ttaaatattt gcctcttctt gaccgggctc atgcttcaca agtttgccgc aactggaacc 240
239   aggtatttca catgcctgac ttgtggagat gttttgaatt tgaactgaat cagccagcta 300
240   catcttattt gaaagctacc catccagagc tgatcaaaca gattattaaa agacattcaa 360
241   accatctaca atatgtcagc ttcaagggtg acagcagcaa ggaatcagct gaagcagctt 420
242   gtgatatact atcgcaactt gtgaattgct ctttaaaaac acttggaactt atttcaactg 480
243   ctcgaccaag ctttatggat ttaccaaagt ctactttat ctctgcactg acagttgtgt 540
244   tcgtaaactc caaatccctg tcttcgctta agatagatga tactccagta gatgatccat 600

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RAW SEQUENCE LISTING ERROR SUMMARY

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Input Set : N:\Crf3\RULE60\10632150.RAW.txt

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:26; Xaa Pos. 218,556,630  
Seq#:29; N Pos. 13,47,68,88,270  
Seq#:30; Xaa Pos. 15,22,28,89  
Seq#:37; N Pos. 45,329,332  
Seq#:38; Xaa Pos. 110,111  
Seq#:51; N Pos. 1733  
Seq#:52; Xaa Pos. 576,586  
Seq#:53; N Pos. 348  
Seq#:54; Xaa Pos. 150,309,340,374  
Seq#:59; N Pos. 471

VERIFICATION SUMMARY

DATE: 02/20/2004

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Input Set : N:\Crf3\RULE60\10632150.RAW.txt

Output Set: N:\CRF4\02202004\J632150.raw

L:964 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:208  
M:341 Repeated in SeqNo=26  
L:1188 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:0  
M:341 Repeated in SeqNo=29  
L:1203 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:0  
M:341 Repeated in SeqNo=30  
L:1374 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:0  
M:341 Repeated in SeqNo=37  
L:1403 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38 after pos.:96  
L:1948 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51 after pos.:1680  
L:2030 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52 after pos.:560  
M:341 Repeated in SeqNo=52  
L:2049 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53 after pos.:300  
L:2101 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54 after pos.:144  
M:341 Repeated in SeqNo=54  
L:2349 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59 after pos.:420